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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/555,529	07/24/2000	PATRICIA KANNOUCHE	192863USOPCT	6934
22850	7590	03/06/2006	EXAMINER	
OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. 1940 DUKE STREET ALEXANDRIA, VA 22314			JOHANNSEN, DIANA B	
			ART UNIT	PAPER NUMBER
			1634	

DATE MAILED: 03/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 09/555,529	Applicant(s) KANNOUCHE ET AL.	
	Examiner Diana B. Johannsen	Art Unit 1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) Responsive to communication(s) filed on 01 September 2005.
- 2a) This action is FINAL. 2b) This action is non-final.
- 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) Claim(s) 30-78 is/are pending in the application.
4a) Of the above claim(s) 43-58, 66-73 and 75-78 is/are withdrawn from consideration.
- 5) Claim(s) _____ is/are allowed.
- 6) Claim(s) 30-42, 59-65 and 74 is/are rejected.
- 7) Claim(s) _____ is/are objected to.
- 8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) The specification is objected to by the Examiner.
- 10) The drawing(s) filed on _____ is/are: a) accepted or b) objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
a) All b) Some * c) None of:
 1. Certified copies of the priority documents have been received.
 2. Certified copies of the priority documents have been received in Application No. _____.
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) Notice of References Cited (PTO-892)
- 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 0203.
- 4) Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) Notice of Informal Patent Application (PTO-152)
- 6) Other: sequence alignments.

FINAL ACTION

1. This action is responsive to the complying complete set of claims filed 01 September 2005, as well as to the Supplemental Response to Election of Species filed 30 September 2003. Any rejections not reiterated in this action have been withdrawn.

This action is FINAL.

2. It is noted that the new title and amendments to the specification filed 15 July 2004 (and re-submitted 01 September 2005) have been entered.

Election/Restriction

3. It is again noted that the Amendment of 10 February 2003 canceled original claims 1-29 (which claims were subject to the Restriction Requirement mailed 08 July 2002), and added new claims 30-78. New claims 30-42, 59-65, and 74-75 are drawn to nucleic acids encoding proteins and fragments thereof, expression vectors, host cells, and nucleic acid detection reagents, and therefore correspond to elected Group I.

4. Newly submitted claims 43-58, 66-73, and 76-78 are directed to inventions that are independent or distinct from the invention originally claimed and elected by Applicant (see the Response to Restriction Requirement filed 08 August 2002) for the following reasons:

- New claims 43-53, 66-73, and 76-78 are drawn to methods for detecting nucleic acids, corresponding to non-elected Group II (original claims 6-12); and

- New claims 54-58 are drawn to methods in which polynucleotides are expressed in cells so as to produce proteins that inhibit cell proliferation, corresponding to non-elected Group VI (original claim 26).

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Applicant has received an action on the merits for the originally presented and elected invention of Group I. As the inventions of claims 43-58, 66-73, and 76-78 correspond to non-elected inventions previously withdrawn from consideration, claims 43-58, 66-73, and 76-78 are also withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

5. Additionally, Applicant's election with traverse of SEQ ID Nos 18, 19, 27, and 28 in the reply filed on 06 June 2003 is acknowledged. The traversal is on the ground(s) that the Office "has not provided adequate reasons and/or examples to support a conclusion of patentable distinctness between the identified groups." The response continues that the statement by the examiner that "each primer pair is characterized by a different combination of particular nucleotide sequences and functions in the amplification of a different target sequence" is "an unsupported conclusion." This is not found persuasive because applicants' own specification provides the sequences of each primer (each of which differs from the other) and exemplifies the fact that each primer pair amplifies a different target sequence, such that the examiner's conclusion is supported by the teachings of applicants' own specification. Further, Applicants' response has provided no specific arguments supporting a conclusion different from that reached by the examiner (for example, applicants have not indicated what they believe might constitute a "special technical feature" shared by all the molecules encompassed by the claims). Accordingly, Applicants' arguments are not persuasive.

The requirement is still deemed proper and is therefore made FINAL.

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It is noted that in the Supplemental Response of 30 September 2003, Applicant clarified the fact that claims 45, 48, 49, 68, 71, 74, 76, and 77 read on the elected primers. Of these claims, only claim 74 is encompassed by elected Group I.

Claim 75, which is encompassed by Group I, does not read on elected primers SEQ ID NOS 18, 19, 27 and/or 28. Accordingly, claim 75 is withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 06 June 2003.

Claim 74 is also withdrawn from consideration to the extent that it is drawn to non-elected sequences (i.e., sequences other than elected primers SEQ ID Nos 18-19 and a "fragment obtained by amplification of a kin17 nucleotide sequence with SEQ ID NO: 18 and SEQ ID NO: 19").

6. This application contains claims 43-58, 66-73, and 75-78 drawn to inventions nonelected with traverse. A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144). See MPEP § 821.01.

7. Applicants' request in the response of 10 February 2003 that non-elected process claims be rejoined at such time as the elected claims are found allowable is noted. However, no claims are allowed at this time.

Declaration under 37 CFR 1.132

8. In view of the cancellation of original claims 1-5, 24-25 and 29, it is noted that the rejections of those claims set forth in the Office action of 09 October 2002 are moot.

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However, it is also noted that the Declaration under 37 CFR 1.132 filed 10 February 2003 is sufficient to disqualify the Kannouche et al reference (Biochimie 79:599-606 [1997]) as prior art under 35 USC 102(a).

Information Disclosure Statement

9. The information disclosure statement filed 10 February 2003 fails to comply with 37 CFR 1.98(a)(2), which requires a legible copy of each cited foreign patent document; each non-patent literature publication or that portion which caused it to be listed; and all other information or that portion which caused it to be listed. Specifically, no copy of reference AAA (M.D. Adams et al) has been provided; accordingly, that reference has not been considered.

Claim Rejections - 35 USC § 112

10. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED

BY APPLICANTS' AMENDMENTS TO THE CLAIMS

11. Claims 39-42 and 64-65 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a new matter rejection.

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While applicants' specification discloses bacteria and particular lines of cells comprising vectors and plasmids that express various kin17 proteins and variants thereof (see, e.g., page 1 and examples throughout the specification), the specification as originally filed does not broadly disclose host cells comprising polynucleotides that encode such proteins, as encompassed by the instant claims. The specification does not refer to or provide any type of limiting definition of the term "host cell," and the claims as written are sufficiently broad so as to encompass any type of cell comprising the claimed polynucleotides in any form (including polynucleotides which are [unlike the molecules exemplified in the specification] free of any type of vector or plasmid construct). It is noted that Applicants have not provided any type of specific reference to locations in the specification that are believed to provide basis for the claims (rather, Applicants merely state that support is found "in Claims 1-29 and the specification as originally filed" (see the response of 10 February 2003)), and the examiner could not identify basis for this subject matter as it is now broadly claimed. Accordingly, claims 39-42 and 64-65 introduce new matter.

12. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

**THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY
APPLICANTS' AMENDMENTS TO THE CLAIMS**

13. Claims 30-42 and 59-65 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

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Claims 30-42 and 49-65 are indefinite over the recitation of the language "kin17 protein which comprises an amino acid sequence wherein amino acids ___ to ___ are deleted in SEQ ID NO:___" in claims 30, 32-34, and 59-60. This language does not make clear the structural requirements of the molecules encompassed by the claims. While the claims make reference to particular amino acids that are "deleted in" a SEQ ID NO, the claims do not otherwise require that the "non-deleted" portion of that SEQ ID NO be present in the claimed molecules. While one of skill in the art could clearly identify a molecule comprising, e.g., the two portions of SEQ ID NO: 26 flanking a particular "deleted" region, it is not clear how one would or could identify molecules encompassed by the claims that do not include the "non-deleted" portion of the SEQ ID NO referenced in the claims. Clarification is required.

Claim Rejections - 35 USC § 101

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY APPLICANTS' AMENDMENTS TO THE CLAIMS

14. 35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

15. Claims 39 and 65 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claims do not sufficiently distinguish over cells that exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring

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products are considered non-statutory subject matter. See *Diamond v. Chakrabarty*, 447 U.S. 303, 206 USPQ 193 (1980).

Specifically, instant claims 39 and 65 as written encompass cells found in nature that comprise wild-type kin17 molecules. While it is noted that claims 31 and 61 (from which claims 39 and 65, respectively, depend) are drawn to "isolated" polynucleotides, as claims 39 and 65 are drawn to host cells that "comprise" such polynucleotides, the polynucleotides encompassed by claims 39 and 65 are not "isolated" molecules.

(With regard to claims 40-42 and 64 (which are also drawn to "host cells"), it is noted that as the host cells of these claims comprise deletion constructs that are not found in nature, these claims meet the requirements of 35 USC 101.)

Claim Rejections - 35 USC § 102

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY APPLICANTS' AMENDMENTS TO THE CLAIMS

It is noted that while applicants' claims previously encompassed nucleic acid fragments of SEQ ID NO: 1 consisting of SEQ ID NO: 18 or SEQ ID NO: 19 (see, e.g., original claim 5), as well as a group of reagents including SEQ ID NO: 18 and SEQ ID NO: 19 (in combination with several other reagents; see, e.g., original claim 29), instant claim 74 encompasses both an isolated polynucleotide comprising SEQ ID NO: 18 and an isolated polynucleotide comprising SEQ ID NO: 19.

16. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

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(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

17. Claim 74 is rejected under 35 U.S.C. 102(b) as being clearly anticipated by Matsuda et al (The Journal of Biological Chemistry 268(33)24950-24958 [1993]).

Matsuda et al disclose double-stranded vectors comprising instant SEQ ID NO: 18 (see entire reference, particularly the "Materials and Methods" section at pages 24950 and Figure 3, particularly nucleotides -270 through -249, which are the reverse complement of instant SEQ ID NO: 18). Accordingly, Matsuda et al clearly anticipate the claimed invention.

18. Claim 74 is rejected under 35 U.S.C. 102(a) as being clearly anticipated by EST database accession no. AI089251 (NCI-CGAP; gb09a11.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone, 8/1998).

EST database accession no. AI089251 discloses a cDNA comprising instant SEQ ID NO : 19 (see entire reference, particularly nucleotides 218-243 of the sequence). Accordingly, EST database accession no. AI089251 clearly anticipates the claimed invention.

Conclusion

19. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure. Sequence alignments are provided to show the identity shared between the nucleic acid of Matsuda et al and instant SEQ ID NO: 18, and the nucleic acid of EST database accession no. AI089251 and instant SEQ ID NO: 19.

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20. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Diana B. Johannsen whose telephone number is 571/272-0744. The examiner can normally be reached on Monday and Thursday, 7:30 am-4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached at 571/272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

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Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



Diana B. Johannsen
Primary Examiner
Art Unit 1634

3/2/06

Sequence alignments

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 12:53:47 ; Search time 116.932 Seconds
(without alignments)
10694.773 Million cell updates/sec

Title: US-09-555-529-18

Perfect score: 1 agaaagtgatcgctgccgtgct 22

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Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: gb_om:.*
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6: gb_pat:.*
7: gb_ph:.*
8: gb_pr:.*
9: gb_ro:.*
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11: gb_by:.*
12: gb_un:.*
13: gb_vi:.*
14: gb_hcg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	1002	6	AX003310 Sequence
3	22	100.0	1117	6	CO722054 Sequence
4	22	100.0	1528	6	AX003308 Sequence
5	22	100.0	1528	8	HSAJ5273 Sequence
6	22	100.0	23065	8	HUMATP5G Sequence
7	22	100.0	174361	8	AL158044 Human DNA
8	22	100.0	194563	14	AL391687 Human DNA
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10	22	18.4	83.6	14	CR847851 Dario rer
11	22	18.4	83.6	5	AC146480 Dario rer
12	22	18.4	83.6	5	AL929558 Zedratish
13	22	18.4	83.6	2	AC018491 Drosophila
14	22	18.4	83.6	2	AE002611 Drosophila
15	22	17.8	80.9	1	AY525807 Streptococcus
16	22	17.8	80.9	5	CR387275 Gallus ga
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ALIGNMENTS

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VERSION
KEYWORDS
SOURCE Homo sapiens (human)
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Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 Angulo-Mora, J.F. and Mauffrey, P. Sequences coding for kiny protein and their applications Patent: WO 9929845-A 18 17-JUN-1999; ANGULO MORA JAIME FRANCISCO (FR); COMMISSARIAT ENERGIE ATOMIQUE (FR)
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RESULT 2
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DEFINITION AX003310
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Query Match 100.0%; Score 22; DB 8; Length 1528;
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RESULT 6
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DEFINITION Homo sapiens gene for ATP synthase gamma-subunit, complete cds.
ACCESSION D16561
VERSION D16561.1 GI:468446
KEYWORDS
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Homidae; Homo.
1 (bases 1 to 23065)
Matsuda, C., Endo, H., Ohta, S. and Kagawa, Y.
Gene structure of human mitochondrial ATP synthase gamma-subunit.
Tissue specificity produced by alternative RNA splicing
J. Biol. Chem. 268 (33), 24950-24958 (1993)
8227057
2 (bases 1 to 23065)
Kagawa, Y.
Direct Submission
Submitted (23-UN-1993) Yasuo Kagawa, Jichi Medical School,
Department of Biochemistry; 3311-1 Yakushiji, Minamikawa-cho,
Tochigi 329-0498, Japan (E-mail: ykagawa@ddbj.nig.ac.jp,
Tel:81-285-44-2111 (ex.3149), Fax:81-285-44-1827)
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FEATURES
source
exon
CDs

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/number=3
12246..14056
/number=3
14057..14261
/number=4
14262..14838
/number=4
14839..14982
/number=5
14983..15093
/number=5
/cons_splICE="(5'site:no, 3'site:yes)
15094..15158
/number=6
15159..17328
/number=6
17329..17484
/number=7
17485..17816
/number=7
17817..17913
/number=8
17914..22027
/number=8
22028..22064
/number=9
22065..22712
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22713..22869
/number=10
22835..22840
22849..22854

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```

Query Match 100.0%; Score 22; DB 8; Length 23065;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

1 AGAAAGTATCGCTGCGCGTGT 22
|||||
3970 AGAAAGTATCGCTGCGCGTGT 3949

```

```

RESULT 7
LOCUS AL158044/c 174361 bp DNA linear PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone Rpl1-264C14 on chromosome 10 contains
the 5' end of the gene for a novel protein (MG10848), the ITH2
gene for Inter-alpha (globulin) inhibitor, H2 polypeptide (H2P),
the KIN gene for KIN, antigenic determinant of reca protein homolog
(mouse), the 3' end of the ATP5C1 gene for ATP synthase, H+
transporting, mitochondrial F1 complex, gamma polypeptide 1
(ATP5C, ATP5C1), a novel gene and two CpG islands, complete
sequence.
ACCESSION AL158044

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: November 26, 2005, 12:58:53 ; Search time 145.336 Seconds
(without alignment)
8370.011 Million cell updates/sec

Title: US-09-555-529-19

Perfect score: 26

Sequence: 1 ggcagaccacattgatgctttaaaga 26

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_hic.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_est7.*
- 9: gb_gss1.*
- 10: gb_gss2.*
- 11: gb_gss3.*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	249	1	AI493544 ch36a10.x
2	26	100.0	328	2	BE091046 PM4-RT072
3	26	100.0	384	1	AA770446 ah89e07.s
4	26	100.0	384	1	AI493563 ch36c10.x
5	26	100.0	386	3	BM661987 UI-B-CX1-
6	26	100.0	469	1	AI087818 coo24a09.x
7	26	100.0	476	1	AI378396 ccf8f05.x
8	26	100.0	485	1	AI089251 qb09a11.x
9	26	100.0	488	3	BM689918 UI-B-CX1-
10	26	100.0	512	5	BQ548883 BK93a03.y
11	26	100.0	516	2	BG944189 ak47e12.x
12	26	100.0	521	2	BE349628 hx58g10.x
13	26	100.0	543	6	CB158664 K-EST0218
14	26	100.0	575	3	BM750112 K-EST0025
15	26	100.0	591	2	BE896845 601437548
16	26	100.0	592	8	CX866354 HESC4_10
17	26	100.0	605	6	CB242639 UI-CP-FNO
18	26	100.0	660	1	AL597250 DKFZ6313A
19	26	100.0	682	1	AV721396 AV721396
20	26	100.0	698	1	AI650375 wa90b01.x
21	26	100.0	701	1	AI807250 wf38f09.x
22	26	100.0	720	7	CK301009 UI-B-EJ1-

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	COMMENT
23	26	100.0	733	5	EX104466						
24	26	100.0	848	1	AL558810						
25	26	100.0	1339	4	CR618602						
26	26	100.0	1396	4	CR595908						
27	25	96.2	723	3	BO186497						
28	25	96.2	259	6	CF526711						
29	24.4	93.8	349	1	AA805923						
30	24.4	93.8	578	5	BU737321						
31	24.4	93.8	691	1	AM028238						
32	24.4	93.8	703	1	AM035210						
33	24.4	93.8	776	2	BF571691						
34	24.4	93.8	786	1	AJ819816						
35	24.4	93.8	864	1	AM037867						
36	24.4	93.8	871	1	AJ819723						
37	24.4	93.8	949	3	BM453332						
38	24.4	93.8	477	1	AJ656645						
39	23	88.5	624	5	BO602324						
40	23	88.5	663	1	AJ660240						
41	23	88.5	682	6	CF795929						
42	23	88.5	1543	4	AY609991						
43	22.8	87.7	800	1	AM038283						
44	22.8	87.7	398	8	H75516						
45	22	84.6									

ALIGNMENTS

AI493544 249 bp mRNA linear EST 30-MAR-1999
 ch36a10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120346 3',
 mRNA sequence.
 AI493544 GI:4394547
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 I (bases 1 to 249)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILMB at:
 www.bio.liml.gov/bbrp/image/image.html
 Insert Length: 841 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 246.
 Location/Qualifiers
 1..249
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2120346"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pan1"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN

Query Match 100.0%; Score 26; DB 1; Length 249;
 Beet Local Similarity 100.0%; Pred. No. 0.42;

the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHP pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HP-9W pool 1: 758280-760583, 772104-774407 Soares NBHP pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Benito Soares and M. Fatima Bonaldo."

ORIGIN Query Match 100.0%; Score 26; DB 1; Length 469; Best Local Similarity 100.0%; Pred. No. 0.46; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGAACCACCAATTGGATGCTTTAAGA 26
 Db 231 GCGAACCACCAATTGGATGCTTTAAGA 256

RESULT 7
 LOCUS A1378396 476 bp mRNA linear EST 18-MAR-1999
 DEFINITION uc78f05.x1 Soares_NhMHPu_S1 Homo sapiens cDNA clone IMAGE:2070753
 3', mRNA sequence.
 ACCESSION A1378396
 VERSION A1378396.1 GI:4188249
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgapbs-r@mail.nih.gov
 This clone is available royally-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 INSERT LENGTH: 625 Std Error: 0.00
 SEG PRIMER: -40up from Gibco
 High quality sequence stop: 442.
 LOCATION/Qualifiers

FEATURES
 source
 1..476
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2070753"
 /issue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares_NhMHPu_S1"
 /note="Organ: mixed (see below); Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBHM19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN Query Match 100.0%; Score 26; DB 1; Length 476; Best Local Similarity 100.0%; Pred. No. 0.46; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGAACCACCAATTGGATGCTTTAAGA 26

Db 218 GCGAACCACCAATTGGATGCTTTAAGA 243

RESULT 8
 LOCUS A1089251 485 bp mRNA linear EST 18-AUG-1998
 DEFINITION db09a11.x1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone
 IMAGE:1695740.3', mRNA sequence.
 ACCESSION A1089251
 VERSION A1089251.1 GI:3428310
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgapbs-r@mail.nih.gov
 This clone is available royally-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 SEG PRIMER: -40m13 fwd. Et from Amersham
 High quality sequence stop: 442.
 LOCATION/Qualifiers

FEATURES
 source
 1..485
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1695740"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Soares_pregnant_uterus_NBHPU"
 /note="Organ: uterus; Vector: pT773-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGAAATTCGCGCCCTTTTCTTTTCTTTTCTTTT 3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

ORIGIN Query Match 100.0%; Score 26; DB 1; Length 485; Best Local Similarity 100.0%; Pred. No. 0.47; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGAACCACCAATTGGATGCTTTAAGA 26
 Db 218 GCGAACCACCAATTGGATGCTTTAAGA 243

RESULT 9
 LOCUS BM689918/c 488 bp mRNA linear EST 28-FEB-2002
 DEFINITION UT-E-CK1-abo-f-09-0-UT.r1 UT-E-CK1 Homo sapiens cDNA clone
 BM689918
 ACCESSION BM689918
 VERSION BM689918.1 GI:19003176
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae; Homo.
 1 (bases 1 to 488)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.